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Figure S1. Related to Figure 2. Phenotypic and functional stability of Liver ILC1 during MCMV challenge.

(a) Flow cytometry gating strategy for identifying Liver ILC1. (b) 4x10<sup>4</sup> liver ILC1 (Lin NK1.1+ CD49b CD200r1+CD11b Ly49H) were sort purified from CD45.1+ mice, adoptively transferred i.v. into Ly49H-deficient CD45.2+ WT hosts, and subsequently infected with MCMV. Histograms show indicated cell surface markers on liver ILC1 and mNK cells from uninfected WT mice and adoptively transferred liver ILC1 recovered 7 days PI. Data are representative of 3 independent experiments with n=3 mice per group.

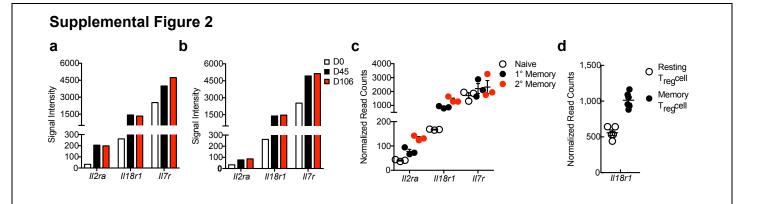


Figure S2. Related to Figure 3. Memory T cell populations increase the expression of cytokine receptors following the resolution of infection.

(a,b) Graph shows average mRNA expression of indicated cytokine receptors in splenic OT-I CD8<sup>+</sup> T Cell sorted from (a) Listeria-OVA and (b) VSV-OVA infected mice at indicated time-points PI, as assessed by microarray (Data provided by Immunological Genome Consortium <sup>54</sup>. (c-d) Graph shows mRNA expression of indicated cytokine receptors by (c) naïve and LCMV experienced primary and secondary memory GP66-CD4<sup>+</sup> T cells post LCMV infection and by (d) resting and inflammation experienced memory Tregs, assed by RNA-sequencing as was previously reported <sup>23</sup>. Data are representative of 2 independent experiments with (c) n=3 and (d) n=5 mice per group. Data are presented as the mean ± SEM.



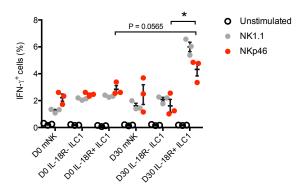
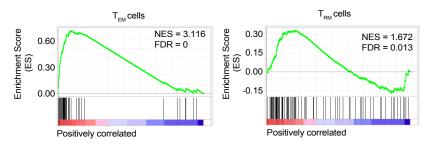
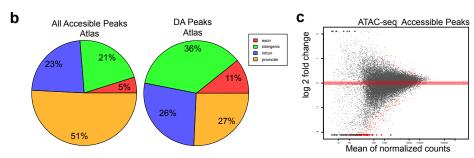


Figure S3. Related to Figure 4. II-18rα<sup>+</sup> ILC1 display enhanced IFN-γ production following stimulation of activating receptors.

WT mice were infected with MCMV (i.p.) and liver was harvested and analyzed 30 days PI. Graph shows percentage of IFN- $\gamma^+$  cells within indicated liver ILC1 populations following plate-bound stimulation with either media alone,  $\alpha$ NKp46, or  $\alpha$ NK1.1 plate-bound antibodies compared to uninfected mice. Data are representative of 3 independent experiments with n=3 mice per group. Samples were compared using a two-tailed Student's t test, and data are presented as the mean  $\pm$  SEM (\*p<0.05).









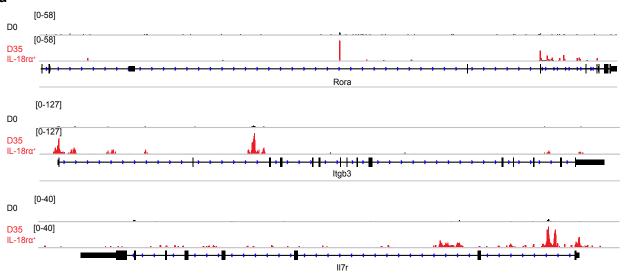


Figure S4. Related to Figure S5. Memory ILC1 have distinct transcriptome and epigenomes compared to naïve ILC1.

(a) Gene set enrichment analysis (GSEA) of genes upregulated in D35 IL-18rα<sup>+</sup> ILC1 over D0 ILC1 from genes upregulated in effector memory T cells (T<sub>EM</sub>) (left) or resident memory T cells (T<sub>EM</sub>) (right) compared to naïve T cells after LCMV infection, assessed by RNA-sequencing as was previously reported<sup>32</sup>. (NES, normalized enrichment score; FDR, false discovery rate; NES, normalized enrichment score assessed by an empirical phenotype based permutation test assuming a null distribution). (b) Absolute numbers and proportion of all peaks (23016 total) and differentially accessible (DA) peaks in peak atlas (373 total, p value less than 0.2). (c) MA plots of differentially accessible regions (red dots) of all peak types comparing D0 vs D35 IL-18ra<sup>+</sup> ILC1. (d) Representative ATAC-sequencing tracks show accessible regions for *Rora*, *Itgb3*, and *Il7r* in naïve and memory ILC1. Y axis depicts normalized counts, while *x* axis displays genomic axis with scale bar. Data are representative of 2 replicate experiments with n=2 samples of n=20 mice per condition. All adjusted p values were indeed determined using DESeq2 and were two-sided.

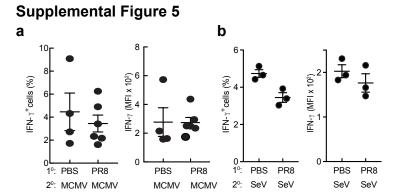


Figure S5. Related to Figure 6. Induction of ILC1 memory is MCMV specific and cannot be formed by other viruses.

.WT mice were injected initially with either PBS or Influenza-PR8 intranasally (i.n.). 28 days PI, mice were subsequently challenged with either MCMV (i.n.) or Sendai virus (Sev) and analyzed 48 hours PI. (a) Quantification of intracellular IFN-γ staining by percentage and MFI of ILC1 at 48 hours following primary and secondary MCMV challenge in i.v. CD45 unlabeled fraction of the lung. (b) Quantification of intracellular IFN-γ staining by percentage and MFI of ILC1 at 48 hours following primary and secondary SeV challenge in i.v. CD45 unlabeled fraction of the lung. Data are representative of 3 independent experiments with (a) n=4 mice and (b) n=3 per group. Data are presented as the mean ± SEM.

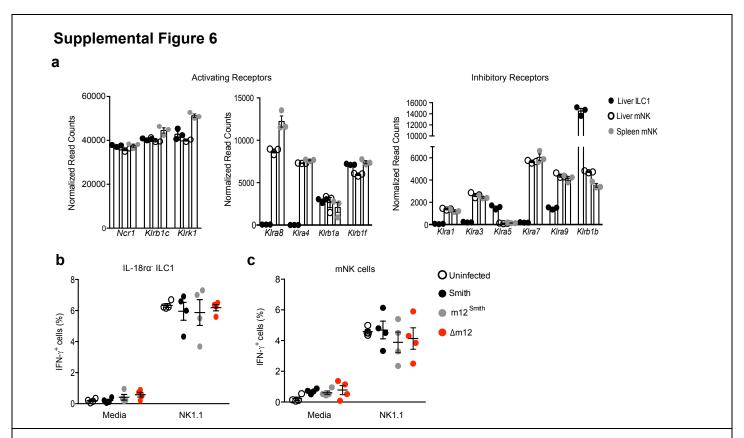


Figure S6. Related to Figure 6. The MCMV-encoded protein m12 does not drive memory formation of IL-18rα<sup>-</sup> ILC1.

(a) Graph shows mRNA expression of indicated Group 1 ILC specific activating and inhibitory receptors in resting liver ILC1, liver mNK, and splenic mNK, obtained by RNA-sequencing as was previously reported <sup>12</sup>. (b-c) WT mice were infected with indicated MCMV strains i.p. and liver ILC1 were analyzed 30 days PI. Quantification of IFN- $\gamma^+$  cells within liver for (b) IL18r $\alpha^-$  ILC1 and (c) mNK following plate-bound stimulation with either media alone or  $\alpha$ NK1.1 antibody. Data are representative of 3 independent experiments with (a) n=3 mice and (b) n=4 per group. Data are presented as the mean  $\pm$  SEM.